

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/507,446

Source:

PT/10

Date Processed by STIC:

9/23/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

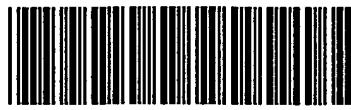
Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202**

Revised 05/17/04



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/507,446

DATE: 09/23/2004
TIME: 11:50:43

Input Set : A:\Sequence Listing PCT JP0302946.txt
Output Set: N:\CRF4\09232004\J507446.raw

3 <110> APPLICANT: GOTO, Hidetsugu
4 NAKANO, Shigeru
6 <120> TITLE OF INVENTION: Structural gene responsible for acetic acid resistance in
acetic acid bacteria, acetic acid bacteria transformed with said gene,
and acetic acid fermentation using said transformations
10 <130> FILE REFERENCE: 4439-4024
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/507,446
C--> 13 <141> CURRENT FILING DATE: 2004-09-13
15 <150> PRIOR APPLICATION NUMBER: PCT/JP03/02946
16 <151> PRIOR FILING DATE: 2003-03-12
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 2016
24 <212> TYPE: DNA
25 <213> ORGANISM: Gluconacetobacter entanii
27 <400> SEQUENCE: 1
28 gatataatg gcagcagcaa gatcgtttag gatctggcct ttgatttact ggcgtcatg 60
30 aattttgtca tggaaatcga ggacacgctc gacgtttccg tgccgcttga cccgctggct 120
32 gatatccgca ccattgtatga tctgctgccc tgcgtatcgct ctctcaagca ggcattctga 180
34 tacaccatgt cgatttctc gaaatatgaa ggccttgcgt cgccttgcgt ggcggtaacg 240
36 gccgatggtg ggcgcaacccc gttcaacgctc gtatcgaaa agcccatatc ctccacggtc 300
38 gggctgatcg aaggcgccga gacgcttctg ttccggacca acaactatct tgggctgagc 360
40 cagtccccgg ccgcgatcga agcgccgtg gaagccgcca gggcttatgg tgcggcaccg 420
42 accggatcgc gcatcgccaa tggcacgcag ggtctgcacc gccagttgga agagcgctg 480
44 tgcacccctc tccgtcgatc gcaactgcattg gtgttttcca cccgttacca gccaatctg 540
46 ggcacgattt cccgactggc gggcaaggac gattatctgc tgcttgcattgc ggacagccat 600
48 gccagcatct atgatggcag ccgccttggc catgcgcagg tcattccgtt ccgtcacaac 660
50 gacgcccattt acctgcataa acgcctgcgc cgccttgcgt gtacgcccgg agcggaaactg 720
52 gtcgtggatc aaggcatctt ttccatgtatg ggcgacgtcg ttcccatggc ggaattcgcg 780
54 gccgtcaagc gggaaaccgg tgcgtatggctg ctggcgatg aagcacatc cttgggtgt 840
56 atgggcgaac atggccgtgg cgtggcgaa tccgacgcgc tggaaatgtt tgcgtatctt 900
58 gtcgtccggc cctttccaa aagccttggc acgggttgcgt gctactgtgt ttccaaaccat 960
60 gccgggctgg acctgtatccg gctgtgtcg cgtccgtaca tggatccaccgc atccctggcg 1020
62 ccggaaatcga tcgcccgcac catggccgcg ctgactgaac tggaaaaccg gccggaaactg 1080
64 cgcgtgcggc tgcgtatggcataa tgcacgcagg cttcatgcac ggcgtgcaggc ggcgggctg 1140
66 cgcaccggcc cgcaggccag tcctgtcgatg tccgtcattc tggatgtatgt ggcgggttgc 1200
68 gtggcgatctt ggaaccggct gctggacctt ggggtttacg tcaacctcgat cctggccct 1260
70 gcaacgcccgg accagcatcc cctgtgcggc acctccgtca tggcgaccga tggccggag 1320
72 cagatagacc gggccgtggc aatcttcgcgatc gttgtacggc gcgagatggg tatcaaccgc 1380
74 gccgcctgaa aaaacctgccc tgccgtatatt tccacagcag atacggcagg cagaccagcg 1440
76 gatgccgttc cggaaaacggc cccagcggca gttcaatgcgatc ggaatgcccgc ctgtatctcc 1500
78 atqcqatata qcqcqccca cttcaaaacq tqaaggcccc cttqaacacq cggctqacat 1560

Does Not Comply
Corrected Diskette Needed
pp.5-6

**Does Not Comply
Corrected Diskette Needed**

file:///C:/CRF4/Outhold/VsrJ507446.htm

9/23/04

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Input Set : A:\Sequence Listing PCT JP0302946.txt
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80	tcagcacg	ccccagccga	ccacgcagcc	accagccttc	gtacatctc	cggcgcagtt	1620									
82	caggtgtc	agctgggtt	attgtatcg	cctcagaccc	gaacggcagg	ccatcgccgc	1680									
84	gccatac	atc	cgccagcagg	cgcctgtacc	gtgcttc	cccctgttagc	1740									
86	gcctgcgg	cc	gttctccaca	cgcagttccg	caccgtta	atgggcgaac	1800									
88	agtagtc	atc	ggccgtgccc	tgtgccggac	ccagggcggc	agcccagcgc	1860									
90	ccaccgcg	cg	gataatgcag	gcaggatgg	catgcgcgc	gtccggttcc	1920									
92	caagcgcac	aggctggcag	aaggctgccc	agaccgtgg	atccaa	ctgaccata	1980									
94	tcatgcgg	cg	gaactgcgt	atggacagga	tggcca	g	2016									
97	<210> SEQ ID NO: 2															
98	<211> LENGTH: 400															
99	<212> TYPE: PRT															
100	<213> ORGANISM: Gluconacetobacter entanii															
102	<400> SEQUENCE: 2															
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105	1			5			10									15
108	Val	Thr	Ala	Asp	Gly	Gly	Arg	Asn	Pro	Phe	Asn	Val	Val	Ile	Glu	Lys
109				20			25									30
112	Pro	Ile	Ser	Ser	Thr	Val	Gly	Leu	Ile	Glu	Gly	Arg	Glu	Thr	Leu	Leu
113				35			40									45
116	Phe	Gly	Thr	Asn	Asn	Tyr	Leu	Gly	Leu	Ser	Gln	Ser	Pro	Ala	Ala	Ile
117				50			55									60
120	Glu	Ala	Ala	Val	Glu	Ala	Ala	Arg	Ala	Tyr	Gly	Val	Gly	Thr	Thr	Gly
121	65				70			75								80
124	Ser	Arg	Ile	Ala	Asn	Gly	Thr	Gln	Gly	Leu	His	Arg	Gln	Leu	Glu	Glu
125					85			90								95
128	Arg	Leu	Cys	Thr	Phe	Phe	Arg	Arg	Arg	His	Cys	Met	Val	Phe	Ser	Thr
129				100			105									110
132	Gly	Tyr	Gln	Ala	Asn	Leu	Gly	Thr	Ile	Ser	Ala	Leu	Ala	Gly	Lys	Asp
133				115			120									125
136	Asp	Tyr	Leu	Leu	Leu	Asp	Ala	Asp	Ser	His	Ala	Ser	Ile	Tyr	Asp	Gly
137				130			135									140
140	Ser	Arg	Leu	Gly	His	Ala	Gln	Val	Ile	Arg	Phe	Arg	His	Asn	Asp	Ala
141	145				150					155						160
144	Asp	Asp	Leu	His	Lys	Arg	Leu	Arg	Arg	Leu	Asp	Gly	Thr	Pro	Gly	Ala
145					165			170								175
148	Lys	Leu	Val	Val	Val	Glu	Gly	Ile	Tyr	Ser	Met	Met	Gly	Asp	Val	Val
149				180			185									190
152	Pro	Met	Ala	Glu	Phe	Ala	Ala	Val	Lys	Arg	Glu	Thr	Gly	Ala	Trp	Leu
153				195			200									205
156	Leu	Ala	Asp	Glu	Ala	His	Ser	Val	Gly	Val	Met	Gly	Glu	His	Gly	Arg
157				210			215				220					
160	Gly	Val	Ala	Glu	Ser	Asp	Gly	Val	Glu	Asp	Asp	Val	Asp	Phe	Val	Val
161	225				230				235							240
164	Gly	Thr	Phe	Ser	Lys	Ser	Leu	Gly	Thr	Val	Gly	Gly	Tyr	Cys	Val	Ser
165					245				250							255
168	Asn	His	Ala	Gly	Leu	Asp	Leu	Ile	Arg	Leu	Cys	Ser	Arg	Pro	Tyr	Met
169					260			265			270					
172	Phe	Thr	Ala	Ser	Leu	Pro	Pro	Glu	Val	Ile	Ala	Ala	Thr	Met	Ala	Ala
173				275			280			285						

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Input Set : A:\Sequence Listing PCT JP0302946.txt
Output Set: N:\CRF4\09232004\J507446.raw

176 Leu Thr Glu Leu Glu Asn Arg Pro Glu Leu Arg Val Arg Leu Met Asp
177 290 295 300
180 Asn Ala Arg Arg Leu His Asp Gly Leu Gln Ala Ala Gly Leu Arg Thr
181 305 310 315 320
184 Gly Pro Gln Ala Ser Pro Val Val Ser Val Ile Leu Asp Asp Val Ala
185 325 330 335
188 Val Ala Val Ala Phe Trp Asn Arg Leu Leu Asp Leu Gly Val Tyr Val
189 340 345 350
192 Asn Leu Ser Leu Pro Pro Ala Thr Pro Asp Gln His Pro Leu Leu Arg
193 355 360 365
196 Thr Ser Val Met Ala Thr His Thr Pro Glu Gln Ile Asp Arg Ala Val
197 370 375 380
200 Glu Ile Phe Ala Val Val Ala Gly Glu Met Gly Ile Asn Arg Ala Ala
201 385 390 395 400
204 <210> SEQ ID NO: 3
205 <211> LENGTH: 1360
206 <212> TYPE: DNA
207 <213> ORGANISM: Acetobacter aceti
209 <400> SEQUENCE: 3
210 gaagacagct tggatgtatc tatccgctc gacaaaactgg ctgatatacg aacgattaat 60
212 gaccttgcgg cttgcattgt tgctctgaaa aacaaaagggt gaggcgttgg tgacatcact 120
214 attttccaaa tttgaaggta cggcaggcgc gctgggttcc gttgtggccg taggcggtcg 180
216 caaccctttt gctgtgtta ttgaaaaacc tgtctttca actgttgaa ttattgaagg 240
218 tcgggaaacg cttcttttg gcaccaataa ctatttgggg cttagtcaat ccaaaaatgc 300
220 cattcaagca gcccacgcagg ctgcccggc atgtggcgta ggcacaaacgg gctcacgcac 360
222 tgcaaattggc acacaatccc tgcacccgaca gcttgaaaaa gatattggcg cgtttttgg 420
224 tcggcgtgat gccatggttt tttccacggg gtatcaggca aacctcggca ttatttccac 480
226 gctggcaggt aaggatgacc acctgtttct ggatgctgat agccacggca gtatctatga 540
228 tggcagccgc ctgagtgca cagaagttat tcgcttccgc cataatgatc cagacaacct 600
230 ttataaacgc cttaaacgc tggatggcac gccaggcgcc aaattgattt tggttgaagg 660
232 catttattcc atgacgggta atgttgcucc gattgcagaa tttgttgcgt taaaaaaaga 720
234 aacaggcgcct tacctgttgg tagatgaagc ccattttttt ggcgtgttgg gtcaaaatgg 780
236 gctgtgtgcc gctgaggctg atggcgttgg agctgtatg gactttgttgcg tcggcacatt 840
238 ttccaaaaggc ttgggcacag ttggcggtt ctgcgtatct gaccatcctg agctggagtt 900
240 tggcgttta aactgccggc cctatatgtt tacggcatcg ctaccgcgg aagttattgc 960
242 tgccacaaacg gctgccttga aagatatgca ggcacatcct gaattgcgtt agcagcttat 1020
244 ggcaaaacgcg cagcaactac atgcagggtt tgtatgatatt gggctaaatg ccagcaaaaca 1080
246 cgcaacccca gttattgccc ttacattgga aacagctgaa gaagctattc ccatgtggaa 1140
248 caggcttttgc gaaactgggtt tttatgtaaa tctcagcctt cctccggcta caccagattc 1200
250 gcccggcttgc ctccgggtt ccgtaatggc caccatcag cccgaacaaa ttgcgcaggc 1260
252 tattgccata ttcaggcagg ctgcggcaga agtaggcgtt accatcacac cctccgctgc 1320
254 ttaaaaaaaaaa gctatgttgcg cttgaatgcc ctttgctgcc 1360
257 <210> SEQ ID NO: 4
258 <211> LENGTH: 404
259 <212> TYPE: PRT
260 <213> ORGANISM: Acetobacter aceti
262 <400> SEQUENCE: 4
264 Met Thr Ser Leu Phe Ser Lys Phe Glu Gly Thr Ala Gly Ala Leu Gly
265 1 5 10 15

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268 Ser Val Val Ala Val Gly Gly Arg Asn Pro Phe Ala Val Val Ile Glu
 269 20 25 30
 272 Lys Pro Val Ser Ser Thr Val Gly Ile Ile Glu Gly Arg Glu Thr Leu
 273 35 40 45
 276 Leu Phe Gly Thr Asn Asn Tyr Leu Gly Leu Ser Gln Ser Lys Asn Ala
 277 50 55 60
 280 Ile Gln Ala Ala Gln Gln Ala Ala Ala Ala Cys Gly Val Gly Thr Thr
 281 65 70 75 80
 284 Gly Ser Arg Ile Ala Asn Gly Thr Gln Ser Leu His Arg Gln Leu Glu
 285 85 90 95
 288 Lys Asp Ile Ala Ala Phe Phe Gly Arg Arg Asp Ala Met Val Phe Ser
 289 100 105 110
 292 Thr Gly Tyr Gln Ala Asn Leu Gly Ile Ile Ser Thr Leu Ala Gly Lys
 293 115 120 125
 296 Asp Asp His Leu Phe Leu Asp Ala Asp Ser His Ala Ser Ile Tyr Asp
 297 130 135 140
 300 Gly Ser Arg Leu Ser Ala Ala Glu Val Ile Arg Phe Arg His Asn Asp
 301 145 150 155 160
 304 Pro Asp Asn Leu Tyr Lys Arg Leu Lys Arg Met Asp Gly Thr Pro Gly
 305 165 170 175
 308 Ala Lys Leu Ile Val Val Glu Gly Ile Tyr Ser Met Thr Gly Asn Val
 309 180 185 190
 312 Ala Pro Ile Ala Glu Phe Val Ala Val Lys Lys Glu Thr Gly Ala Tyr
 313 195 200 205
 316 Leu Leu Val Asp Glu Ala His Ser Phe Gly Val Leu Gly Gln Asn Gly
 317 210 215 220
 320 Arg Gly Ala Ala Glu Ala Asp Gly Val Glu Ala Asp Val Asp Phe Val
 321 225 230 235 240
 324 Val Gly Thr Phe Ser Lys Ser Leu Gly Thr Val Gly Gly Tyr Cys Val
 325 245 250 255
 328 Ser Asp His Pro Glu Leu Glu Phe Val Arg Leu Asn Cys Arg Pro Tyr
 329 260 265 270
 332 Met Phe Thr Ala Ser Leu Pro Pro Glu Val Ile Ala Ala Thr Thr Ala
 333 275 280 285
 336 Ala Leu Lys Asp Met Gln Ala His Pro Glu Leu Arg Lys Gln Leu Met
 337 290 295 300
 340 Ala Asn Ala Gln Gln Leu His Ala Gly Phe Val Asp Ile Gly Leu Asn
 341 305 310 315 320
 344 Ala Ser Lys His Ala Thr Pro Val Ile Ala Val Thr Leu Glu Thr Ala
 345 325 330 335
 348 Glu Glu Ala Ile Pro Met Trp Asn Arg Leu Leu Glu Leu Gly Val Tyr
 349 340 345 350
 352 Val Asn Leu Ser Leu Pro Pro Ala Thr Pro Asp Ser Arg Pro Leu Leu
 353 355 360 365
 356 Arg Cys Ser Val Met Ala Thr His Thr Pro Glu Gln Ile Ala Gln Ala
 357 370 375 380
 360 Ile Ala Ile Phe Arg Gln Ala Ala Ala Glu Val Gly Val Thr Ile Thr
 361 385 390 395 400
 364 Pro Ser Ala Ala

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Input Set : A:\Sequence Listing PCT JP0302946.txt
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368 <210> SEQ ID NO: 5
369 <211> LENGTH: 30
370 <212> TYPE: DNA
C--> 371 <213> ORGANISM: *Artificial* Sequence
W--> 373 <220> FEATURE:
W--> 373 <223> OTHER INFORMATION:
W--> 373 <400> 5

374 ctggctgcct gtatcgtctc tctcaaggcag
377 <210> SEQ ID NO: 6
378 <211> LENGTH: 30
379 <212> TYPE: DNA
C--> 380 <213> ORGANISM: *Artificial* Sequence
W--> 382 <220> FEATURE:
W--> 382 <223> OTHER INFORMATION:
W--> 382 <400> 6

383 acggctgcag ctggcttgcc tgccgtatct
386 <210> SEQ ID NO: 7
387 <211> LENGTH: 30
388 <212> TYPE: DNA
C--> 389 <213> ORGANISM: *Artificial* Sequence
W--> 391 <220> FEATURE:
W--> 391 <223> OTHER INFORMATION:
W--> 391 <400> 7

392 ggcaaaccctc ggcattatttt ccacgctggc
395 <210> SEQ ID NO: 8
396 <211> LENGTH: 29
397 <212> TYPE: DNA
C--> 398 <213> ORGANISM: *Artificial* Sequence
W--> 400 <220> FEATURE:
W--> 400 <223> OTHER INFORMATION:
W--> 400 <400> 8

401 gcgaatctgg ttagccgga ggaaggctg
404 <210> SEQ ID NO: 9
405 <211> LENGTH: 30
406 <212> TYPE: DNA
C--> 407 <213> ORGANISM: *Artificial* Sequence
W--> 409 <220> FEATURE:
W--> 409 <223> OTHER INFORMATION:
W--> 409 <400> 9

410 gccagcgtgg aaataatgcc gaggtttgcc
413 <210> SEQ ID NO: 10
414 <211> LENGTH: 29
415 <212> TYPE: DNA
C--> 416 <213> ORGANISM: *Artificial* Sequence
W--> 418 <220> FEATURE:
W--> 418 <223> OTHER INFORMATION:
W--> 418 <400> 10

419 cagccttcctt ccggctacac cagattcgc

→ see p. 6 for error explanation

same error

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\Sequence Listing PCT JP0302946.txt
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Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:5,6,7,8,9,10

VERIFICATION SUMMARY

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Input Set : A:\Sequence Listing PCT JP0302946.txt
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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:371 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:373 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:373 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:373 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:373
L:380 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:382 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:382 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:382 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:382
L:389 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:391 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:391 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:391 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:391
L:398 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:400 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:400 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:400 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:400
L:407 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:409 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:409 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:409 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:409
L:416 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:418 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:418 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:418 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:418